



IFWO

## RAW SEQUENCE LISTING

DATE: 02/03/2004

PATENT APPLICATION: US/10/763,276

TIME: 10:53:44

Input Set : N:\Cr3\RULE60\10763276.RAW.txt

Output Set: N:\CRF4\01302004\J763276.raw

1 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
 2 <120> TITLE OF INVENTION: Substance which inhibits binding of information  
 3 transfer molecule for 1175-tyrosine phosphorylated KDR/Flk-1  
 4 and usages of the same  
 5 <130> FILE REFERENCE: 249-199  
 6 <140> CURRENT APPLICATION NUMBER: 10/763,276  
 7 <141> CURRENT FILING DATE: 2004-01-26  
 8 <150> PRIOR APPLICATION NUMBER: US/09/969,037B  
 9 <151> PRIOR FILING DATE: 2002-08-30  
 10 <150> PRIOR APPLICATION NUMBER: JP 2000-303694  
 11 <151> PRIOR FILING DATE: 2000-10-03  
 12 <150> PRIOR APPLICATION NUMBER: US 60/263,512  
 13 <151> PRIOR FILING DATE: 2001-01-24  
 14 <160> NUMBER OF SEQ ID NOS: 7  
 15 <170> SOFTWARE: PatentIn Ver. 2.1  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 11  
 19 <212> TYPE: PRT  
 20 <213> ORGANISM: Artificial Sequence  
 21 <220> FEATURE:  
 22 <221> NAME/KEY: Phosphorylation  
 23 <222> LOCATION: 7  
 24 <220> FEATURE:  
 25 <223> OTHER INFORMATION: an antigen peptide  
 26 <400> SEQUENCE: 1  
 27 Cys Asp Gly Lys Asp Tyr Ile Val Leu Pro Ile  
 28 1 5 10  
 30 <210> SEQ ID NO: 2  
 31 <211> LENGTH: 11  
 32 <212> TYPE: PRT  
 33 <213> ORGANISM: Artificial Sequence  
 34 <220> FEATURE:  
 35 <223> OTHER INFORMATION: a peptide SEQ ID NO:1 without phosphorylation  
 36 <400> SEQUENCE: 2  
 37 Cys Asp Gly Lys Asp Tyr Ile Val Leu Pro Ile  
 38 1 5 10  
 40 <210> SEQ ID NO: 3  
 41 <211> LENGTH: 27  
 42 <212> TYPE: DNA  
 43 <213> ORGANISM: Artificial Sequence  
 44 <220> FEATURE:  
 45 <223> OTHER INFORMATION: a primer for replacing KDR/Flk-1 tyr 1175 to phenylalanine  
 46 <400> SEQUENCE: 3

ENTERED

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47      gatggcaaaag acttcattgt tcttccc                27
49 <210> SEQ ID NO: 4
50 <211> LENGTH: 27
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial Sequence
53 <220> FEATURE:
54 <223> OTHER INFORMATION: a primer for replacing KDR/Flk-1 tyr 1214 to phe
55 <400> SEQUENCE: 4
56      cccaaattcc atttcgacaa cacagca                27
58 <210> SEQ ID NO: 5
59 <211> LENGTH: 20
60 <212> TYPE: DNA
61 <213> ORGANISM: Artificial Sequence
62 <220> FEATURE:
63 <223> OTHER INFORMATION: a primer for replacing KDR/Flk-1 tyr 801 to phe
64 <400> SEQUENCE: 5
65      gacaggcttc ttgtccatcg                20
67 <210> SEQ ID NO: 6
68 <211> LENGTH: 20
69 <212> TYPE: PRT
70 <213> ORGANISM: Human
71 <400> SEQUENCE: 6
72      Gln Gly Lys Asp Tyr Val Gly Ala Ile Pro Val Asp Leu Lys Arg Arg
73      1          5          10          15
74      Leu Asp Ser Ile
75      20
77 <210> SEQ ID NO: 7
78 <211> LENGTH: 1356
79 <212> TYPE: PRT
80 <213> ORGANISM: Human
81 <400> SEQUENCE: 7
82      Met Gln Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu
83      1          5          10          15
84      Thr Arg Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro
85      20          25          30
86      Arg Leu Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr
87      35          40          45
88      Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro
89      50          55          60
90      Asn Asn Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser
91      65          70          75          80
92      Asp Gly Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn
93      85          90          95
94      Asp Thr Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser
95      100         105         110
96      Val Ile Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser
97      115         120         125
98      Val Ser Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys
99      130         135         140

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```

100  Thr Val Val Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser
101  145                150                155                160
102  Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg
103                165                170                175
104  Ile Ser Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile
105                180                185                190
106  Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser
107                195                200                205
108  Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr
109                210                215                220
110  Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu
111  225                230                235                240
112  Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile
113                245                250                255
114  Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu
115                260                265                270
116  Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe
117                275                280                285
118  Leu Ser Thr Leu Thr Ile Asp Gly Ile Thr Arg Ser Asp Gln Gly Leu
119                290                295                300
120  Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr
121  305                310                315                320
122  Phe Val Arg Val His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly Met
123                325                330                335
124  Glu Ser Leu Val Glu Ala Thr Val Gly Glu Arg Val Arg Ile Pro Ala
125                340                345                350
126  Lys Tyr Leu Gly Tyr Pro Pro Pro Glu Ile Lys Trp Tyr Lys Asn Gly
127                355                360                365
128  Ile Pro Leu Glu Ser Asn His Thr Ile Lys Ala Gly His Val Leu Thr
129                370                375                380
130  Ile Met Glu Val Ser Glu Arg Asp Thr Gly Asn Tyr Thr Val Ile Leu
131  385                390                395                400
132  Thr Asn Pro Ile Ser Lys Glu Lys Gln Ser His Val Val Ser Leu Val
133                405                410                415
134  Val Tyr Val Pro Pro Gln Ile Gly Glu Lys Ser Leu Ile Ser Pro Val
135                420                425                430
136  Asp Ser Tyr Gln Tyr Gly Thr Thr Gln Thr Leu Thr Cys Thr Val Tyr
137                435                440                445
138  Ala Ile Pro Pro Pro His His Ile His Trp Tyr Trp Gln Leu Glu Glu
139                450                455                460
140  Glu Cys Ala Asn Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro Tyr
141  465                470                475                480
142  Pro Cys Glu Glu Trp Arg Ser Val Glu Asp Phe Gln Gly Gly Asn Lys
143                485                490                495
144  Ile Glu Val Asn Lys Asn Gln Phe Ala Leu Ile Glu Gly Lys Asn Lys
145                500                505                510
146  Thr Val Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr
147                515                520                525
148  Lys Cys Glu Ala Val Asn Lys Val Gly Arg Gly Glu Arg Val Ile Ser

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149	530	535	540
150	Phe His Val Thr Arg Gly Pro Glu Ile Thr Leu Gln Pro Asp Met Gln		
151	545	550	555
152	Pro Thr Glu Gln Glu Ser Val Ser Leu Trp Cys Thr Ala Asp Arg Ser		
153		565	570
154	Thr Phe Glu Asn Leu Thr Trp Tyr Lys Leu Gly Pro Gln Pro Leu Pro		
155		580	585
156	Ile His Val Gly Glu Leu Pro Thr Pro Val Cys Lys Asn Leu Asp Thr		
157		595	600
158	Leu Trp Lys Leu Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile		
159		610	615
160	Leu Ile Met Glu Leu Lys Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr		
161		625	630
162	Val Cys Leu Ala Gln Asp Arg Lys Thr Lys Lys Arg His Cys Val Val		
163		645	650
164	Arg Gln Leu Thr Val Leu Glu Arg Val Ala Pro Thr Ile Thr Gly Asn		
165		660	665
166	Leu Glu Asn Gln Thr Thr Ser Ile Gly Glu Ser Ile Glu Val Ser Cys		
167		675	680
168	Thr Ala Ser Gly Asn Pro Pro Pro Gln Ile Met Trp Phe Lys Asp Asn		
169		690	695
170	Glu Thr Leu Val Glu Asp Ser Gly Ile Val Leu Lys Asp Gly Asn Arg		
171		705	710
172	Asn Leu Thr Ile Arg Arg Val Arg Lys Glu Asp Glu Gly Leu Tyr Thr		
173		725	730
174	Cys Gln Ala Cys Ser Val Leu Gly Cys Ala Lys Val Glu Ala Phe Phe		
175		740	745
176	Ile Ile Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Ile Ile Ile Leu		
177		755	760
178	Val Gly Thr Ala Val Ile Ala Met Phe Phe Trp Leu Leu Val Ile		
179		770	775
180	Ile Leu Arg Thr Val Lys Arg Ala Asn Gly Gly Glu Leu Lys Thr Gly		
181		785	790
182	Tyr Leu Ser Ile Val Met Asp Pro Asp Glu Leu Pro Leu Asp Glu His		
183		805	810
184	Cys Glu Arg Leu Pro Tyr Asp Ala Ser Lys Trp Glu Phe Pro Arg Asp		
185		820	825
186	Arg Leu Lys Leu Gly Lys Pro Leu Gly Arg Gly Ala Phe Gly Gln Val		
187		835	840
188	Ile Glu Ala Asp Ala Phe Gly Ile Asp Lys Thr Ala Thr Cys Arg Thr		
189		850	855
190	Val Ala Val Lys Met Leu Lys Glu Gly Ala Thr His Ser Glu His Arg		
191		865	870
192	Ala Leu Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly His His Leu		
193		885	890
194	Asn Val Val Asn Leu Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu		
195		900	905
196	Met Val Ile Val Glu Phe Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu		
197		915	920
			925

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```

198 Arg Ser Lys Arg Asn Glu Phe Val Pro Tyr Lys Thr Lys Gly Ala Arg
199      930      935      940
200 Phe Arg Gln Gly Lys Asp Tyr Val Gly Ala Ile Pro Val Asp Leu Lys
201      945      950      955      960
202 Arg Arg Leu Asp Ser Ile Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly
203      965      970      975
204 Phe Val Glu Glu Lys Ser Leu Ser Asp Val Glu Glu Glu Glu Ala Pro
205      980      985      990
206 Glu Asp Leu Tyr Lys Asp Phe Leu Thr Leu Glu His Leu Ile Cys Tyr
207      995      1000      1005
208 Ser Phe Gln Val Ala Lys Gly Met Glu Phe Leu Ala Ser Arg Lys Cys
209      1010      1015      1020
210 Ile His Arg Asp Leu Ala Arg Asn Ile Leu Leu Ser Glu Lys Asn
211      1025      1030      1035      1040
212 Val Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asp
213      1045      1050      1055
214 Pro Asp Tyr Val Arg Lys Gly Asp Ala Arg Leu Pro Leu Lys Trp Met
215      1060      1065      1070
216 Ala Pro Glu Thr Ile Phe Asp Arg Val Tyr Thr Ile Gln Ser Asp Val
217      1075      1080      1085
218 Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Ser Leu Gly Ala Ser
219      1090      1095      1100
220 Pro Tyr Pro Gly Val Lys Ile Asp Glu Glu Phe Cys Arg Arg Leu Lys
221      1105      1110      1115      1120
222 Glu Gly Thr Arg Met Arg Ala Pro Asp Tyr Thr Thr Pro Glu Met Tyr
223      1125      1130      1135
224 Gln Thr Met Leu Asp Cys Trp His Gly Glu Pro Ser Gln Arg Pro Thr
225      1140      1145      1150
226 Phe Ser Glu Leu Val Glu His Leu Gly Asn Leu Leu Gln Ala Asn Ala
227      1155      1160      1165
228 Gln Gln Asp Gly Lys Asp Tyr Ile Val Leu Pro Ile Ser Glu Thr Leu
229      1170      1175      1180
230 Ser Met Glu Glu Asp Ser Gly Leu Ser Leu Pro Thr Ser Pro Val Ser
231      1185      1190      1195      1200
232 Cys Met Glu Glu Glu Glu Val Cys Asp Pro Lys Phe His Tyr Asp Asn
233      1205      1210      1215
234 Thr Ala Gly Ile Ser Gln Tyr Leu Gln Asn Ser Lys Arg Lys Ser Arg
235      1220      1225      1230
236 Pro Val Ser Val Lys Thr Phe Glu Asp Ile Pro Leu Glu Glu Pro Glu
237      1235      1240      1245
238 Val Lys Val Ile Pro Asp Asp Asn Gln Thr Asp Ser Gly Met Val Leu
239      1250      1255      1260
240 Ala Ser Glu Glu Leu Lys Thr Leu Glu Asp Arg Thr Lys Leu Ser Pro
241      1265      1270      1275      1280
242 Ser Phe Gly Gly Met Val Pro Ser Lys Ser Arg Glu Ser Val Ala Ser
243      1285      1290      1295
244 Glu Gly Ser Asn Gln Thr Ser Gly Tyr Gln Ser Gly Tyr His Ser Asp
245      1300      1305      1310
246 Asp Thr Asp Thr Thr Val Tyr Ser Ser Glu Glu Ala Glu Leu Leu Lys

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 02/03/2004  
PATENT APPLICATION:    US/10/763,276      TIME: 10:53:45

Input Set : N:\Crf3\RULE60\10763276.RAW.txt  
Output Set: N:\CRF4\01302004\J763276.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:3; Line(s) 45

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/763,276

DATE: 02/03/2004

TIME: 10:53:45

Input Set : N:\Crf3\RULE60\10763276.RAW.txt

Output Set: N:\CRF4\01302004\J763276.raw